

SEQUENCE LISTING

<110> FARWICK, Mike

HUTHMACHER, Klaus

PFEFFERLE, Walter

BATHE, Brigitte

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE RODA PROTEIN

<130> 212532US0

<150> DE10044943.3

<151> 2000-09-12

<150> DE10132947.4

<151> 2001-07-06

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1761

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (238)..(1560)

<223>

<400> 1
gaatgaagct ggcaccttgt cactcaagga atcctgtgaa aacggtacgt ctttcaaatt 60
ggatgattta ccggcatctg ttgcggttag tgctgcagga ttaccgtctg ggctgtatga 120
cgaggtccag gcgcaaagtc aacggctggc tgctcaagct ttgccagtgt gcgtgaactt 180
agaagtaaca accgggtggcg atagaaacga acccgagtc aattgtaggg aggtctc 237
atg aac acg ctt gaa cga tta aag ctt cgt cgc acg gaa atg tgg ctg 285
Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu
5 10 15
ctg ata ctt gcc aca ctc gtt gtg tcg atc atg ttc atc agc ctc gag 333
Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu
20 25 30
ctg gcc atg gcc aat gag ttg ggt acc cat att ttg atg ctg atg ggc 381
Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
35 40 45
gga tat atc ggt atc ttc atc gtc gcg cac cta gcc atg gca tgg gtg 429
Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
50 55 60
gcg ccg ttt gct gat caa atc atg ctg cct gtg gtg gcg gtg ctc aat 477
Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
65 70 75 80
ggc att ggt ttg gtg atg att tat cgc ctt gat gag gcc acg ggc tac 525
Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
85 90 95
agc acg gtc aat agc caa ttg atg tgg acg gtt gtt ggc gtc acg ctg 573
Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
100 105 110
atg gtg gct gtg ttg ttg ctg ttg cgt gat tac aag tcg ctt tcg cgt 621
Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
115 120 125
tat tcc tac ctc ctc ggt gtg gtg ggc atc gtg ctg ctg gcg ctg cct 669
Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
130 135 140

ctc	gtg	tgg	ccg	cag	cca	ggc	ggc	gtg	gaa	gcc	cgc	atc	tgg	att	tgg	717
Leu	Val	Trp	Pro	Gln	Pro	Gly	Gly	Val	Glu	Ala	Arg	Ile	Trp	Ile	Trp	
145					150				155						160	
ctt	gga	cct	ttc	tcc	atc	cag	cca	ggt	gag	ttc	tcc	aag	att	tgg	ctg	765
Leu	Gly	Pro	Phe	Ser	Ile	Gln	Pro	Gly	Glu	Phe	Ser	Lys	Ile	Leu	Leu	
				165					170					175		
ctg	ctg	ttc	ttt	gct	cag	ctg	cta	gcc	acc	aag	cgt	gct	ttg	ttt	act	813
Leu	Leu	Phe	Phe	Ala	Gln	Leu	Leu	Ala	Thr	Lys	Arg	Ala	Leu	Phe	Thr	
			180					185					190			
gtt	gcg	ggc	tac	cgt	ttc	ctc	ggc	atg	gat	ttc	cct	cgt	ttg	cgt	gac	861
Val	Ala	Gly	Tyr	Arg	Phe	Leu	Gly	Met	Asp	Phe	Pro	Arg	Leu	Arg	Asp	
		195					200					205				
ctc	gcg	ccg	att	ctt	gtg	gtg	tgg	gcg	ttg	gct	att	ttg	atc	atg	gct	909
Leu	Ala	Pro	Ile	Leu	Val	Val	Trp	Ala	Leu	Ala	Ile	Leu	Ile	Met	Ala	
	210				215						220					
ggc	gcc	aac	gac	ttc	ggt	cct	gca	ctg	ctg	ctt	ttc	act	acc	ggt	ttg	957
Gly	Ala	Asn	Asp	Phe	Gly	Pro	Ala	Leu	Leu	Leu	Phe	Thr	Thr	Val	Leu	
225					230					235					240	
ggc	atg	gtg	tac	ctg	gct	acc	ggc	cgt	ggt	tcc	tgg	ctg	ttg	att	ggt	1005
Ala	Met	Val	Tyr	Leu	Ala	Thr	Gly	Arg	Gly	Ser	Trp	Leu	Leu	Ile	Gly	
				245					250					255		
gct	gtg	ttg	gtg	gct	gtc	ggc	gcg	ttc	gcg	gtg	tac	caa	ggt	tca	agc	1053
Ala	Val	Leu	Val	Ala	Val	Gly	Ala	Phe	Ala	Val	Tyr	Gln	Val	Ser	Ser	
			260					265					270			
aag	att	cag	gaa	cgc	gtg	caa	aac	ttc	gtg	gat	cct	gtg	gcc	cac	tat	1101
Lys	Ile	Gln	Glu	Arg	Val	Gln	Asn	Phe	Val	Asp	Pro	Val	Ala	His	Tyr	
		275					280					285				
gac	acc	acc	ggt	tac	cag	ctg	tcc	cag	tcc	ttg	ttt	ggc	atg	agt	tgg	1149
Asp	Thr	Thr	Gly	Tyr	Gln	Leu	Ser	Gln	Ser	Leu	Phe	Gly	Met	Ser	Trp	
		290				295					300					
ggc	gga	atc	acc	ggc	acc	ggc	att	ggt	cag	ggt	tac	ccc	aac	atg	atc	1197
Gly	Gly	Ile	Thr	Gly	Thr	Gly	Ile	Gly	Gln	Gly	Tyr	Pro	Asn	Met	Ile	
305					310					315					320	
cct	gtc	gtg	cac	tcg	gac	ttc	att	ctc	gca	gcc	att	ggt	gag	gag	ctt	1245
Pro	Val	Val	His	Ser	Asp	Phe	Ile	Leu	Ala	Ala	Ile	Gly	Glu	Glu	Leu	
				325					330					335		
ggt	ctg	att	ggc	ctg	gcg	gcc	atc	atc	gtg	ctg	ttt	ggt	gtg	ttt	gtc	1293
Gly	Leu	Ile	Gly	Leu	Ala	Ala	Ile	Ile	Val	Leu	Phe	Gly	Val	Phe	Val	
			340					345					350			

acc cgc ggt atg cgc acc gct acc ctg gct cgt gac agc tac gga aag 1341
Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
355 360 365

ctc gtg gca tct ggt ctg tcg atg acc atc atg atc cag att ttc gtc 1389
Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
370 375 380

gtc gtg gca ggt att tct tca ctg atg ccc atg aca ggt ttg acc act 1437
Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
385 390 395 400

cgc ttt atg tcc cag ggt ggt tca tcc ctg atg gct aac tac att ctg 1485
Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
405 410 415

atg gcc atc atc ttg cgt att tct gac agt gcc cgc cga cct gtc atg 1533
Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
420 425 430

tcc aag caa gca tcg gag gtg gct gcg tgaaccgctc gattcgaatc 1580
Ser Lys Gln Ala Ser Glu Val Ala Ala
435 440

acatccctct tctctttgct cctgatcttg gtgctcgtag caaacctcac ctggattcag 1640

gccttttaggg acgatgatct tgctcagaac ccaactgaacg cacgtgggtt cctggaggcg 1700

aaatccactc cgcggtggaca gatttcaact ggtggccaag tactcgcaga gtcctcccag 1760

g 1761

<210> 2

<211> 441

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu
1 5 10 15

Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu
20 25 30

Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
 35 40 45
 Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
 50 55 60
 Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
 65 70 75 80
 Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
 85 90 95
 Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
 100 105 110
 Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
 115 120 125
 Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
 130 135 140
 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
 145 150 155 160
 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
 165 170 175
 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
 180 185 190
 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp
 195 200 205
 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
 210 215 220
 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
 225 230 235 240

Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
245 250 255

Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser
260 265 270

Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
275 280 285

Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
290 295 300

Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
305 310 315 320

Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
325 330 335

Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
340 345 350

Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
355 360 365

Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
370 375 380

Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
385 390 395 400

Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
405 410 415

Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
420 425 430

Ser Lys Gln Ala Ser Glu Val Ala Ala
435 440

<210> 3
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic DNA
 <400> 3
 gatctagagt caattgtagg gaggtctc 28

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic DNA
 <400> 4
 ctctgcagga gggatgtgat tcgaatcg 28